

OIR

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/551,380A

CRF Processing Date: 10/15/2001  
Edited by: me  
Verified by: me (STIC stat)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;  
☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

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Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

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#11/11/01

11-15-01

## RAW SEQUENCE LISTING

DATE: 10/15/2001

PATENT APPLICATION: US/09/551,380A

TIME: 21:11:34

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10152001\I551380A.raw

3 <110> APPLICANT: CHANG, Donald C  
4 LUO, Qian  
6 <120> TITLE OF INVENTION: Modified Fluorescent Proteins  
8 <130> FILE REFERENCE: MLY-5  
10 <140> CURRENT APPLICATION NUMBER: US 09/551,380A  
11 <141> CURRENT FILING DATE: 2000-04-18  
13 <160> NUMBER OF SEQ ID NOS: 55  
15 <170> SOFTWARE: PatentIn version 3.1  
17 <210> SEQ ID NO: 1  
18 <211> LENGTH: 39  
19 <212> TYPE: DNA  
20 <213> ORGANISM: Artificial Sequence  
22 <220> FEATURE:  
23 <223> OTHER INFORMATION: PCR Primer  
25 <220> FEATURE:  
26 <221> NAME/KEY: CDS  
27 <222> LOCATION: (3)..(38)  
28 <223> OTHER INFORMATION:  
30 <400> SEQUENCE: 1  
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32 Pro Ile Gly Asp Glu Val Asp Gly Pro Val Leu Leu  
33 1 5 10  
35 <210> SEQ ID NO: 2  
36 <211> LENGTH: 12  
37 <212> TYPE: PRT  
38 <213> ORGANISM: Artificial Sequence  
40 <220> FEATURE:  
41 <223> OTHER INFORMATION: PCR Primer  
43 <400> SEQUENCE: 2  
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45 1 5 10  
47 <210> SEQ ID NO: 3  
48 <211> LENGTH: 39  
49 <212> TYPE: DNA  
50 <213> ORGANISM: artificial sequence  
52 <220> FEATURE:  
53 <223> OTHER INFORMATION: PCR primer  
55 <400> SEQUENCE: 3  
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58 <210> SEQ ID NO: 4  
59 <211> LENGTH: 4  
60 <212> TYPE: PRT  
61 <213> ORGANISM: Homo sapiens  
63 <400> SEQUENCE: 4  
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65 1  
67 <210> SEQ ID NO: 5

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68 <211> LENGTH: 720
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70 <213> ORGANISM: artificial sequence
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73 <223> OTHER INFORMATION: Possible cleavage site
75 <220> FEATURE:
76 <221> NAME/KEY: CDS
77 <222> LOCATION: (1)..(714)
78 <223> OTHER INFORMATION:
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83 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
84 1          5          10          15
85 gaa tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga gag      96
86 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
87          20          25          30
88 ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc      144
89 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
90          35          40          45
91 act act gga aaa cta cct gtt cca tgg cca aca ctt gtc act act ttc      192
92 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
93          50          55          60
94 act tat ggt gtt caa tgc ttt tca aga tac cca gat cat atg aaa cag      240
95 Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
96 65          70          75          80
97 cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa aga      288
98 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
99          85          90          95
100 act ata ttt ttc aaa gat gac ggg aac tac aag aca cgt gct gaa gtc      336
101 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
102          100          105          110
103 aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt att      384
104 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
105          115          120          125
106 gat ttt aaa gaa gat gga aac att ctt gga cac aaa ttg gaa tac aac      432
107 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
108          130          135          140
109 tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat gga      480
110 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
111 145          150          155          160
112 atc aaa gtt aac ttc aaa att aga cac aac att gaa gat gga agc gtt      528
113 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
114          165          170          175
115 caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc cct      576
116 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
117          180          185          190
118 gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt tcg      624
119 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
120          195          200          205

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121 aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt gta      672
122 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
123      210      215      220
124 aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa taataa      720
125 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
126 225      230      235
128 <210> SEQ ID NO: 6
129 <211> LENGTH: 238
130 <212> TYPE: PRT
131 <213> ORGANISM: artificial sequence
133 <220> FEATURE:
134 <223> OTHER INFORMATION: Possible cleavage site
136 <400> SEQUENCE: 6
137 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
138 1      5      10      15
140 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
141      20      25      30
143 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
144      35      40      45
146 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
147      50      55      60
149 Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
150 65      70      75      80
152 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
153      85      90      95
155 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
156      100      105      110
158 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
159      115      120      125
161 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
162      130      135      140
164 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
165 145      150      155      160
167 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
168      165      170      175
170 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
171      180      185      190
173 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
174      195      200      205
176 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
177      210      215      220
179 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
180 225      230      235
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183 <211> LENGTH: 4
184 <212> TYPE: PRT
185 <213> ORGANISM: Homo sapiens
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190 1  
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193 <211> LENGTH: 4  
194 <212> TYPE: PRT  
195 <213> ORGANISM: artificial sequence  
197 <220> FEATURE:  
198 <223> OTHER INFORMATION: Caspase cleavage site  
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201 Asp Glu His Asp  
202 1  
204 <210> SEQ ID NO: 9  
205 <211> LENGTH: 4  
206 <212> TYPE: PRT  
207 <213> ORGANISM: artificial sequence  
209 <220> FEATURE:  
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213 Trp Glu His Asp  
214 1  
216 <210> SEQ ID NO: 10  
217 <211> LENGTH: 4  
218 <212> TYPE: PRT  
219 <213> ORGANISM: artificial sequence  
221 <220> FEATURE:  
222 <223> OTHER INFORMATION: Caspase cleavage site  
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226 1  
228 <210> SEQ ID NO: 11  
229 <211> LENGTH: 4  
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235 Val Glu Ile Asp  
236 1  
238 <210> SEQ ID NO: 12  
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240 <212> TYPE: PRT  
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243 <220> FEATURE:  
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248 1  
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251 <211> LENGTH: 4  
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253 <213> ORGANISM: artificial sequence  
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256 <223> OTHER INFORMATION: Caspase cleavage site  
258 <400> SEQUENCE: 13  
259 Leu Glu His Asp  
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263 <211> LENGTH: 3  
264 <212> TYPE: PRT  
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267 <220> FEATURE:  
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271 Glu Val Asp  
272 1  
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275 <211> LENGTH: 3  
276 <212> TYPE: PRT  
277 <213> ORGANISM: artificial sequence  
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284 1  
286 <210> SEQ ID NO: 16  
287 <211> LENGTH: 4  
288 <212> TYPE: PRT  
289 <213> ORGANISM: artificial sequence  
291 <220> FEATURE:  
292 <223> OTHER INFORMATION: Possible cleavage site  
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295 Asp Glu Asp Asp  
296 1  
298 <210> SEQ ID NO: 17  
299 <211> LENGTH: 5  
300 <212> TYPE: PRT  
301 <213> ORGANISM: artificial sequence  
303 <220> FEATURE:  
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308 1 5  
310 <210> SEQ ID NO: 18  
311 <211> LENGTH: 2  
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313 <213> ORGANISM: artificial sequence  
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316 <223> OTHER INFORMATION: Possible cleavage site  
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319 Glu Val  
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VERIFICATION SUMMARY

DATE: 10/15/2001

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